



SEQUENCE LISTING

<110> He, et al.

<120> Antibodies to Interleukin-1 Beta Converting Enzyme Like Apoptosis
Protease 3 and 4

<130> PF140C2

<140> 09/895,263

<141> 2001-07-02

<150> 08/334,251

<151> 1994-11-01

<160> 14

<170> PatentIn version 3.2

<210> 1

<211> 1369

<212> DNA

<213> Homo sapiens

<400> 1

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ggccaacttg gcagagcgcg cggccagctt tgcagagagc gccctccagg gactatgcgt      120
gcggggacac gggtcgcttt gggctcttcc acccctgcgg agcgcactac cccgagccag      180
gggcggtgca agccccgccc ggccctaccc agggcggtc ctcctccgc agcgccgaga      240
cttttagttt cgctttcgct aaaggggccc cagacccttg ctgcggagcg acggagagag      300
actgtgccag tcccagccgc cctaccgccg tgggaacgat ggcagatgat cagggctgta      360
ttgaagagca gggggttgag gattcagcaa atgaagattc agtggatgct aagccagacc      420
ggtcctcggt tgtaccgtcc ctcttcagta agaagaagaa aaatgtcacc atgcgatcca      480
tcaagaccac cggggaccga gtgcctacat atcagtacaa catgaatttt gaaaagctgg      540
gcaaatgcat cataataaac aacaagaact ttgataaagt gacaggtatg ggcgttcgaa      600
acggaacaga caaatatgcc gaggcgtctt tcaagtgctt ccgaagcctg ggttttgacg      660
tgattgtcta taatgactgc tcttgtgcca agatgcaaga tctgcttaaa aaagctttctg      720
aagaggacca tacaaatgcc gcttgcctcg cctgcatcct cttaagccat ggagaagaaa      780
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gggatagatg caaaaccctt ttagagaaac ccaaactctt cttcattcag gcttgccgag      900
ggaccgagct tgatgatgcc atccaggccg actcggggcc catcaatgac acagatgcta      960
atcctcgata caagatccca gtggaagctg acttctctct cgcctattcc acggttccag     1020
gctattactc gtggaggagc ccaggaagag gctcctgggt tgtgcaagcc ctctgctcca     1080
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tcctggagga gcacggaaaa gacctggaaa tcatgcagat cctcaccagg gtgaatgaca 1140
 gagttgccag gcactttgag tctcagtctg atgaccaca cttccatgag aagaagcaga 1200
 tccccgtgtg ggtctccatg ctcaccaagg aactctactt cagtcaatag ccatatcagg 1260
 ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc 1320
 ttgaaatatt cagaaattct ccaggatttt aatttcagga aaatgtatt 1369

<210> 2
 <211> 303
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser
 1 5 10 15

Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val
 20 25 30

Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile
 35 40 45

Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe
 50 55 60

Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys
 65 70 75 80

Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala
 85 90 95

Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn
 100 105 110

Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu
 115 120 125

Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His
 130 135 140

Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys
 145 150 155 160

Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu

	165		170		175										
Lys	Pro	Lys	Leu	Phe	Phe	Ile	Gln	Ala	Cys	Arg	Gly	Thr	Glu	Leu	Asp
			180					185					190		
Asp	Ala	Ile	Gln	Ala	Asp	Ser	Gly	Pro	Ile	Asn	Asp	Thr	Asp	Ala	Asn
		195					200					205			
Pro	Arg	Tyr	Lys	Ile	Pro	Val	Glu	Ala	Asp	Phe	Leu	Phe	Ala	Tyr	Ser
	210					215					220				
Thr	Val	Pro	Gly	Tyr	Tyr	Ser	Trp	Arg	Ser	Pro	Gly	Arg	Gly	Ser	Trp
225					230					235					240
Phe	Val	Gln	Ala	Leu	Cys	Ser	Ile	Leu	Glu	Glu	His	Gly	Lys	Asp	Leu
				245					250					255	
Glu	Ile	Met	Gln	Ile	Leu	Thr	Arg	Val	Asn	Asp	Arg	Val	Ala	Arg	His
			260					265					270		
Phe	Glu	Ser	Gln	Ser	Asp	Asp	Pro	His	Phe	His	Glu	Lys	Lys	Gln	Ile
		275					280					285			
Pro	Cys	Val	Val	Ser	Met	Leu	Thr	Lys	Glu	Leu	Tyr	Phe	Ser	Gln	
	290					295					300				

<210> 3
 <211> 1159
 <212> DNA
 <213> Homo sapiens

<400> 3	
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ctcataacctg tggtctgtgta tccgtggcca cagctggttg gcgtcgccctt gaaatcccag	120
gccgtgagga gttagcgagc cctgctcaca ctccggcgctc tggttttcgg tgggtgtgcc	180
ctgcacctgc ctcttcccgc attctcatta ataaagggtat ccatggagaa cactgaaaac	240
tcagtggatt caaaatccat taaaattttg gaaccaaaga tcatacatgg aagcgaatca	300
atggactctg gaatatccct ggacaacagt tataaaatgg attatcctga gatgggttta	360
tgtataataa ttaataataa gaattttcat aaaagcactg gaatgacatc tcggtctggt	420
acagatgtcg atgcagcaaa cctcaggga acattcagaa acttgaaata tgaagtcagg	480
aataaaaaatg atcttacacg tgaagaaatt gtggaattga tgcgtgatgt ttctaaagaa	540
gatcacagca aaaggagcag ttttgtttgt gtgcttctga gccatggtga agaaggaata	600

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atttttggaa caaatggacc tgttgacctg aaaaaataa caaacttttt cagaggggat      660
cgttgtagaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca      720
gaactggact gtggcattga gacagacagt ggtgttgatg atgacatggc gtgtcataaa      780
ataccagtgg aggccgactt cttgtatgca tactccacag cacctgggta ttattcttgg      840
cgaaattcaa aggatggctc ctggttcatc cagtcgcttt gtgccatgct gaaacagtat      900
gccgacaagc ttgaatttat gcacattctt acccggggta accgaaaggt ggcaacagaa      960
tttgagtctt tttcctttga cgctactttt catgcaaaga aacagattcc atgtattggt    1020
tccatgctca caaaagaact ctatttttat cactaaagaa atggttgggt ggtgggtttt    1080
tttagtttgt atgccaagtg agaagatggt atatttgggt actgtatttc cctctcattg    1140
gggacctact ctcatgctg                                     1159

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<210> 4
<211> 277
<212> PRT
<213> Homo sapiens

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<400> 4

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Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
1          5          10          15

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```

Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
          20          25          30

```

```

Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
          35          40          45

```

```

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
          50          55          60

```

```

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65          70          75          80

```

```

Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
          85          90          95

```

```

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
          100          105          110

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```

Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
          115          120          125

```

Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
 130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
 145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
 165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
 180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
 195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
 210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
 225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
 245 250 255

His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
 260 265 270

Leu Tyr Phe Tyr His
 275

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains a Bam HI restriction enzyme site (underlined) followed
 by 18 nucleotides of ICE-LAP-3 coding sequence starting from the
 presumed terminal amino acid of the processed protein codon

<400> 5
 gatcgatcc atgcgtgcgg ggacacgggt c

31

<210> 6
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains complementary sequences to an Xba I site followed by 21 nucleotides of ICE-LAP-3

<400> 6
 gtactctaga tcattcaccc tgggtggagga t 31

<210> 7
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains a Bam HI restriction enzyme site followed by 18 nucleotides of ICE-LAP-4 coding sequence starting from the presumed terminal amino acid of the processed protein codon

<400> 7
 gatcggatcc atggagaaca ctgaaaactc a 31

<210> 8
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains complementary sequences to an Xba I site followed by 21 nucleotides of ICE-LAP-4

<400> 8
 gtactctaga ttagtgataa aaatagagtt c 31

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains the ICE-LAP-3 translational initiation site ATG followed by 5 nucleotides of ICE-LAP-3 coding sequence starting from the initiation codon

<400> 9
 gactatgcgt gcggggacac gg 22

<210> 10
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-3 coding sequence, not including the stop codon

<400> 10

aatcaagcgt agtctgggac gtcgtatggg tattcacct ggtggaggat ttg 53

<210> 11
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Contains the ICE-LAP-4 translational initiation site, ATG,
followed by 15 nucleotides of ICE-LAP-4 coding sequence starting
from the initiation codon

<400> 11
accatggaga aactgaaaa c 21

<210> 12
<211> 53
<212> DNA
<213> Artificial sequence

<220>
<223> Contains translation stop codon, HA tag and the last 21
nucleotides of the ICE-LAP-4 coding sequence, not including the
stop codon

<400> 12
aatcaagcgt agtctgggac gtcgtatggg tagtgataaa aatagagttc ttt 53

<210> 13
<211> 503
<212> PRT
<213> Caenorhabditis elegans

<400> 13

Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met
1 5 10 15

Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala
20 25 30

Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly
35 40 45

Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg
50 55 60

Gly Asp Val Ala Phe Asp Ala Phe Tyr Asp Ala Leu Arg Ser Thr Gly
65 70 75 80

His Glu Gly Leu Ala Glu Val Leu Glu Pro Leu Ala Arg Ser Val Asp
85 90 95

Ser Asn Ala Val Glu Phe Glu Cys Pro Met Ser Pro Ala Ser His Arg
100 105 110

Arg Ser Arg Ala Leu Ser Pro Ala Gly Tyr Thr Ser Pro Thr Arg Val
115 120 125

His Arg Asp Ser Val Ser Ser Val Ser Ser Phe Thr Ser Tyr Gln Asp
130 135 140

Ile Tyr Ser Arg Ala Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser
145 150 155 160

Ser Asp Arg His Asn Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser
165 170 175

Gln Pro Ser Ser Ala Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly
180 185 190

Tyr Ser Ser Ser Arg Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr
195 200 205

Gln Tyr Ile Phe His Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr
210 215 220

Ile Ser Arg Val Phe Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser
225 230 235 240

Pro Arg Gly Met Cys Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met
245 250 255

Pro Thr Arg Asn Gly Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu
260 265 270

Phe Arg Cys Met Gly Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly
275 280 285

Arg Gly Met Leu Leu Thr Ile Arg Asp Phe Ala Lys His Glu Ser His
290 295 300

Gly Asp Ser Ala Ile Leu Val Ile Leu Ser His Gly Glu Glu Asn Val
305 310 315 320

Ile Ile Gly Val Asp Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp
325 330 335

Leu Leu Asn Ala Ala Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Ile
 340 345 ~ 350

Val Phe Val Gln Ala Cys Arg Gly Glu Arg Arg Asp Asn Gly Phe Pro
 355 360 365

Val Leu Asp Ser Val Asp Gly Val Pro Ala Phe Leu Arg Arg Gly Trp
 370 375 380

Asp Asn Arg Asp Gly Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro
 385 390 395 400

Gln Val Gln Gln Val Trp Arg Lys Lys Pro Ser Gln Ala Asp Ile Leu
 405 410 415

Ile Ala Tyr Ala Thr Thr Ala Gln Tyr Val Ser Trp Arg Asn Ser Ala
 420 425 430

Arg Gly Ser Trp Phe Ile Gln Ala Val Cys Glu Val Phe Ser Thr His
 435 440 445

Ala Lys Asp Met Asp Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys
 450 455 460

Val Ala Cys Gly Phe Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln
 465 470 475 480

Met Pro Glu Met Thr Ser Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro
 485 490 495

Glu Ala Arg Asn Ser Ala Val
 500

<210> 14
 <211> 404
 <212> PRT
 <213> Homo sapiens

<400> 14

Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser
 1 5 10 15

Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr
 20 25 30

Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
 35 40 45

Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
 50 55 60

Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
 65 70 75 80

Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly
 85 90 95

Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro
 100 105 110

Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly
 115 120 125

Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile
 130 135 140

Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser
 145 150 155 160

Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile
 165 170 175

Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu
 180 185 190

Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala
 195 200 205

Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His
 210 215 220

Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg
 225 230 235 240

Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu
 245 250 255

Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser
 260 265 270

Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Asp
 275 280 285

Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn
 290 295 300

Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys
 305 310 315 320

Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp
 325 330 335

Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg
 340 345 350

Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu
 355 360 365

Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala
 370 375 380

Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu
 385 390 395 400

Phe Pro Gly His